CLAIMS

1. Factor RecA with an amino acid sequence that is at least identical to 96% of the amino acid sequence listed in SEQ ID NO. 2.

2. Factor according to claim 1 with an amino acid sequence that is increasingly preferably identical to at least 96.5%, 97%, 97.5%, 98%, 98.5%, 99%, 99.5% and quite particularly preferably 100% identical to the amino acid sequence listed in SEQ ID No. 2.

3. Factor RecA, encoded from a nucleic acid, whose nucleotide sequence is at least 85% identical with the nucleotide sequence listed in SEQ ID NO. 1.

4. Factor according to claim 3, encoded from a nucleic acid, whose nucleotide sequence is increasingly preferably identical to at least 87.5%, 90%, 92.5%, 95%, 96%, 97%, 98%, 99% and quite particularly preferably 100% identical of the nucleotide sequence listed in SEQ ID No. 1.

5. Nucleic acid encoding for a factor RecA, whose nucleotide sequence is at least 85% identical with the nucleotide sequence listed in SEQ ID NO. 1.

6. Nucleic acid according to claim 5, whose nucleotide sequence is increasingly preferably identical to at least 87.5%, 90%, 92.5%, 95%, 96%, 97%, 98%, 99% and quite particularly preferably 100% identical of the nucleotide sequence listed in SEQ ID NO. 1.

7. Nucleic acid according to claim 5 or 6, encoding for a factor RecA according to one of claims 1 to 4.

8. Use of nucleic acid that encodes for a factor RecA for the functional inactivation of the gene *recA* in a gram-positive bacterium that is not *Bacillus megaterium*.

9. Use according to claim 8, wherein a nucleic acid that encodes for a non-active protein is introduced with a point mutation.

10. Use according to claim 8, wherein a nucleic acid with a deletion mutation or insertion mutation is employed, preferably comprising each of the boundary sequences that comprise at least 70 to 150 nucleic acid positions of the region encoding for the protein.

11. Use according to claim 8, wherein nucleic acids with a total of two nucleic acid segments are employed that each comprise at least 70 to 150 nucleic acid positions and thereby at least partially, preferably completely flank the region encoding for the protein.

12. Use according to one of claims 8 to 11, wherein it concerns a nucleic acid according to one of claims 5 to 7 and/or a nucleic acid whose nucleotide sequence matches with the nucleotide sequence listed in SEQ ID NO. 31 in the positions 369 to 1415 to at least 1045, preferably at least 1046, quite particularly preferably 1047 of these 1047 positions, or concerns the at least partially non-encoding flanking regions to these nucleic acids.

13. Use according to one of claims 8 to 12, wherein the gram-positive bacterium, preferably one of the genera *Clostridium* or *Bacillus,* is naturally capable of sporulation and a gene from the phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

14. Use according to claim 13, wherein the inactivated gene from the phase IV sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB* or *yqfD* or concerns a homologous gene to this, preferably in the case of *B.*

subtilis the gene is *yqfD*, in the case of *Bacillus licheniformis* is the gene *spoIV* and in all other cases is a homologous gene to this.

15. Use according to claim 13 or 14, wherein exactly one gene from the phase IV of the sporulation is functionally inactivated.

16. Use according to claim 14 or 15, wherein the functional inactivation of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB, yqfD* or *spoIV* or of each of their homologous genes occurs with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof, preferably with the help of parts that comprise at least 70 to 150 contiguous nucleic acid positions, particularly preferably with the help of two such parts that surround a part of the gene located between them.

17. Gram-positive bacterium that is not *Bacillus megaterium* in which the gene *recA* is functionally inactivated.

18. Gram-positive bacterium according to claim 17, wherein the functional inactivation is effected through point mutagenesis, partial deletion or insertion or total deletion of the encoding region for the complete protein.

19. Gram-positive bacterium according to claim 17 or 18, wherein the functional inactivation is effected through a nucleic acid according to one of claims 5 to 7 and/or a nucleic acid whose nucleotide sequence matches with the nucleotide sequence listed in SEQ ID NO. 31 in the positions 369 to 1415 to at least 1045, preferably at least 1046, quite particularly preferably 1047 of these 1047 positions, or is effected through the at least partially non-encoding flanking regions to these nucleic acids.

20. Gram-positive bacterium according to one of claims 17 to 19, preferably one of the genera *Clostridium* or *Bacillus*, which is naturally capable of sporulation and by which a gene from the phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

21. Gram-positive bacterium according to claim 20, wherein the inactivated gene from the phase IV of the sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB* or *yqfD* or concerns a homologous gene to this, preferably in the case of *B. subtilis* the gene is *yqfD*, in the case of *Bacillus licheniformis* is the gene *spoIV* and in all other cases is a homologous gene to this.

22. Gram-positive bacterium according to claim 20 or 21, wherein exactly one gene from the phase IV of the sporulation is functionally inactivated.

23. Gram-positive bacterium according to claim 21 or 22, wherein the functional inactivation of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB, yqfD* or *spoIV* or of each of their homologous genes is effected with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof, preferably with the help of parts that comprise at least 70 to 150 contiguous nucleic acid positions, particularly preferably with the help of two such parts that surround a part of the gene located between them.

24. Gram-positive bacterium according to one of claims 17 to 23, wherein it concerns one of the genera *Clostridium* or *Bacillus*, in particular one of the species *Bacillus subtilis, B. licheniformis, B. amyloliquefaciens, B. stearothermophilus, B. globigii, B. clausii* or *B. lentus*, and quite particularly a strain of *B. licheniformis*.

25. Process for fermenting a gram-positive bacterium according to one of claims 17 to 24.

26. Process according to claim 25 for the manufacture of a product of value, in particular a low molecular weight compound or a protein.

27. Process according to claim 26, wherein the low molecular weight compound concerns a natural product, a nutritional supplement or a pharmaceutically relevant compound.

28. Process according to claim 26, wherein the protein concerns an enzyme, in particular an enzyme from the group of the α-amylases, proteases, cellulases, lipases, oxidoreductases, peroxidases, laccases, oxidases and hemicellulases.

29. Use of the factor RecA according to one of claims 1 to 4 and/or a RecA that matches with the amino acid sequence listed in SEQ ID NO. 32 in at least 347, preferably 348 of the 348 amino acid positions shown there, in a molecular biological reaction approach.

30. Use according to claim 29 for stabilizing single stranded DNA, particularly in a DNA polymerization, in recombination processes *in vitro*, or for converting double stranded DNA into single stranded DNA or vice versa.

31. Vector, comprising a nucleic acid according to one of claims 5 to 7.

32. Vector according to claim 31, wherein it concerns an expression vector.

33. Process for the manufacture of a factor RecA according to one of claims 1 to 4.

34. Process according to claim 33, under addition of a nucleic acid according to one of claims 5 to 7, preferably an expression vector according to claim 32, further preferably by fermentation of a host comprising this nucleic acid or these expression vectors.

35. Use of the nucleic acid encoding for a factor RecA according to one of claims 1 to 4 for expressing this factor.

36. Use according to claim 35 to manufacture this factor itself, particularly in a process according to claim 34, or to modulate molecular biological activities of the cells in question, in particular in recombination processes *in vivo*.

37. Use of the nucleic acid encoding for a factor RecA according to one of claims 5 to 7 and/or a nucleic acid encoding for a factor RecA whose nucleotide sequence matches with the nucleotide sequence listed in SEQ ID NO. 31 in positions 369 to 1415 to at least 1045, preferably at least 1046, particularly preferably 1047 of these 1047 positions, for the inactivation of this factor of the gene *recA* in an *in vitro* approach, in particular through interaction with an associated nucleic acid.

38. A nucleic acid according to SEQ ID NO. 25 to 30 encoding for a partial sequence of *recA* or for a neighboring partial sequence with *recA in vivo*, preferably located less than 1000 bp, particularly preferably less than 500 bp away.

39. Use of at least one, preferably at least two nucleic acids orientated against one another according to SEQ ID NO. 25 to 30 for the amplification of an *in vivo* DNA region enclosed thereby.

40. Use according to claim 39 for the amplification of a *recA* gene.

41. Use according to claim 39 or 40 in the context of a process according to one of claims 8 to 16.

42. Use according to one of claims 39 to 41 for the production of a gram-positive bacterium according to one of claims 17 to 24.

43. A nucleic acid according to SEQ ID NO. 19 to 24 encoding for a partial sequence of *spoIV* or for a neighboring partial sequence with *spoIV in*

vivo, preferably located less than 1000 bp, particularly preferably less than 500 bp away.

44. Use of at least one, preferably at least two nucleic acids orientated against one another according to SEQ ID NO. 25 to 30 for the amplification of an *in vivo* DNA region enclosed thereby.

45. Use according to claim 44 for the amplification of a *spoIV* gene.

46. Use according to claim 44 or 45 in the context of a process according to one of claims 13 to 16.

47. Use according to one of claims 44 to 46 for the production of a gram-positive bacterium according to one of claims 20 to 24.